Title: A multi-region discrete time chain binomial model for infectious disease transmission

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Abstract:

Conventional mathematical models of infectious diseases frequently overlook the spatial spread of the disease concentrating only on local transmission. However, spatial propagation of various diseases have been noted between geographical regions mainly due to the movement of infectious individuals from one region to another. In this work, we propose a multi-region discrete time chain binomial framework to model dependencies between the multiple infection time series from neighbouring regions. It is assumed that the infection counts in each region at various time points is not only governed by local transmissions but also by interactions of individuals between spatial units. Effect of intervention strategies like vaccination campaigns used in disease control and various other socio-demographic factors like, live births, population density, vaccination coverage, disruption in disease surveillance due to covid have been taken into account while modelling the multiple infection time series. For estimating this multi-region chain-binomial model with tunable sparsity, an appropriate likelihood function maximization approach regularized with an l1- type constraint is proposed. Simulation results considering effects of seasonal pattern in disease outbreaks, out of sync outbreaks in connected geographical regions, variations in reporting rates in connecting regions; have been considered to depict realistic disease scenarios. Forecasting of infections and effect of spatial heterogeneity on future infections have also been studied. A real world application based on measles counts from adjoining spatial regions is presented to motivate the proposed modelling approach.